What is claimed is:

1. An isolated 14275, 54420, 8797, 27439, 68730, 69112 or 52908 nucleic acid molecule selected from the group consisting of:
   a) a nucleic acid molecule comprising a nucleotide sequence which is at least 80% identical to the nucleotide sequence of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49;
   b) a nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49;
   c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48;
   d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48;
   e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49, or a complement thereof, under stringent conditions;
   f) a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49, and
   g) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48.
2. The isolated nucleic acid molecule of claim 1, which is the nucleotide sequence SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49.
3. A host cell which contains the nucleic acid molecule of claim 1.
4. An isolated 14275, 54420, 8797, 27439, 68730, 69112 or 52908 polypeptide selected from the group consisting of:
   a) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 80% identical to a nucleic acid

comprising the nucleotide sequence of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49;

b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49, or a complement thereof under stringent conditions;

c) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48; and

d) the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48.

5. An antibody which selectively binds to a polypeptide of claim 4.

6. The polypeptide of claim 4, further comprising heterologous amino acid sequences.

7. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48,

b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48;

c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49; and

d) the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48;

comprising culturing the host cell of claim 3 under conditions in which the nucleic acid molecule is expressed.

8. A method for detecting the presence of a nucleic acid molecule of claim 1 or a polypeptide encoded by the nucleic acid molecule in a sample, comprising:

a) contacting the sample with a compound which selectively hybridizes to the nucleic acid molecule of claim 1 or binds to the polypeptide encoded by the nucleic acid molecule; and

b) determining whether the compound hybridizes to the nucleic acid or binds to the polypeptide in the sample.

9. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 or binds to a polypeptide encoded by the nucleic acid molecule and instructions for use.

10. A method for identifying a compound which binds to a polypeptide or modulates the activity of the polypeptide of claim 4 comprising the steps of:

a) contacting a polypeptide, or a cell expressing a polypeptide of claim 4 with a test compound; and

b) determining whether the polypeptide binds to the test compound or determining the effect of the test compound on the activity of the polypeptide.

11. A method for modulating the activity of a polypeptide of claim 4 comprising contacting the polypeptide or a cell expressing the polypeptide with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

12. A method for identifying a compound capable of treating a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, comprising assaying the ability of the compound to modulate 14275, 54420, 8797, 27439, 68730, 69112 or 52908 nucleic acid expression or 14275, 54420, 8797, 27439, 68730, 69112 or 52908 polypeptide activity, thereby identifying a compound capable of treating a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity.

13. A method of identifying a nucleic acid molecule associated with a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, comprising:

a) contacting a sample from a subject with a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49 defined in claim 2; and

b) detecting the presence of a nucleic acid molecule in the sample that hybridizes to the probe, thereby identifying a nucleic acid molecule

associated with a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity.

14. A method of identifying a polypeptide associated with a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, comprising:

a) contacting a sample comprising polypeptides with a 14275, 54420, 8797, 27439, 68730, 69112 or 52908 polypeptide defined in claim 4; and

b) detecting the presence of a polypeptide in the sample that binds to the 14275, 54420, 8797, 27439, 68730, 69112 or 52908 binding partner, thereby identifying the polypeptide associated with a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity.

15. A method of identifying a subject having a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, comprising:

a) contacting a sample obtained from the subject comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49 defined in claim 2; and

b) detecting the presence of a nucleic acid molecule in the sample that hybridizes to the probe, thereby identifying a subject having a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity.

16. A method for treating a subject having a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, or a subject at risk of developing a disorder characterized by aberrant 14275, 54420, 8797, 27439, 68730, 69112 or 52908 activity, comprising administering to the subject a 14275, 54420, 8797, 27439, 68730, 69112 or 52908 modulator of the nucleic acid molecule defined in claim 1 or the polypeptide encoded by the nucleic acid molecule or contacting a cell with a 14275, 54420, 8797, 27439, 68730, 69112 or 52908 modulator.

17. The method of claim 16, wherein the 14275, 54420, 8797, 27439, 68730, 69112 or 52908 modulator is a small molecule; peptide; phosphopeptide;anti-14275, 54420, 8797, 27439, 68730, 69112 or 52908 antibody; a 14275, 54420, 8797, 27439, 68730, 69112 or 52908 polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, or a fragment thereof; a 14275, 54420, 8797, 27439, 68730, 69112 or 52908 polypeptide comprising an amino acid sequence which is at least 90

percent identical to the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4; or an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49 at 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C.

18. The method of claim 16, wherein the 14275, 54420, 8797, 27439, 68730, 69112 or 52908 modulator is

a) an antisense 14275, 54420, 8797, 27439, 68730, 69112 or 52908 nucleic acid molecule;

b) is a ribozyme;

c) the nucleotide sequence of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49 or a fragment thereof;

d) a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4;

e) a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 5, 14, 17, 33, 36 or 48, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1, 4, 6, 13, 15, 16, 18, 32, 34, 35, 37, 47 or 49 at 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C; or

f) a gene therapy vector.